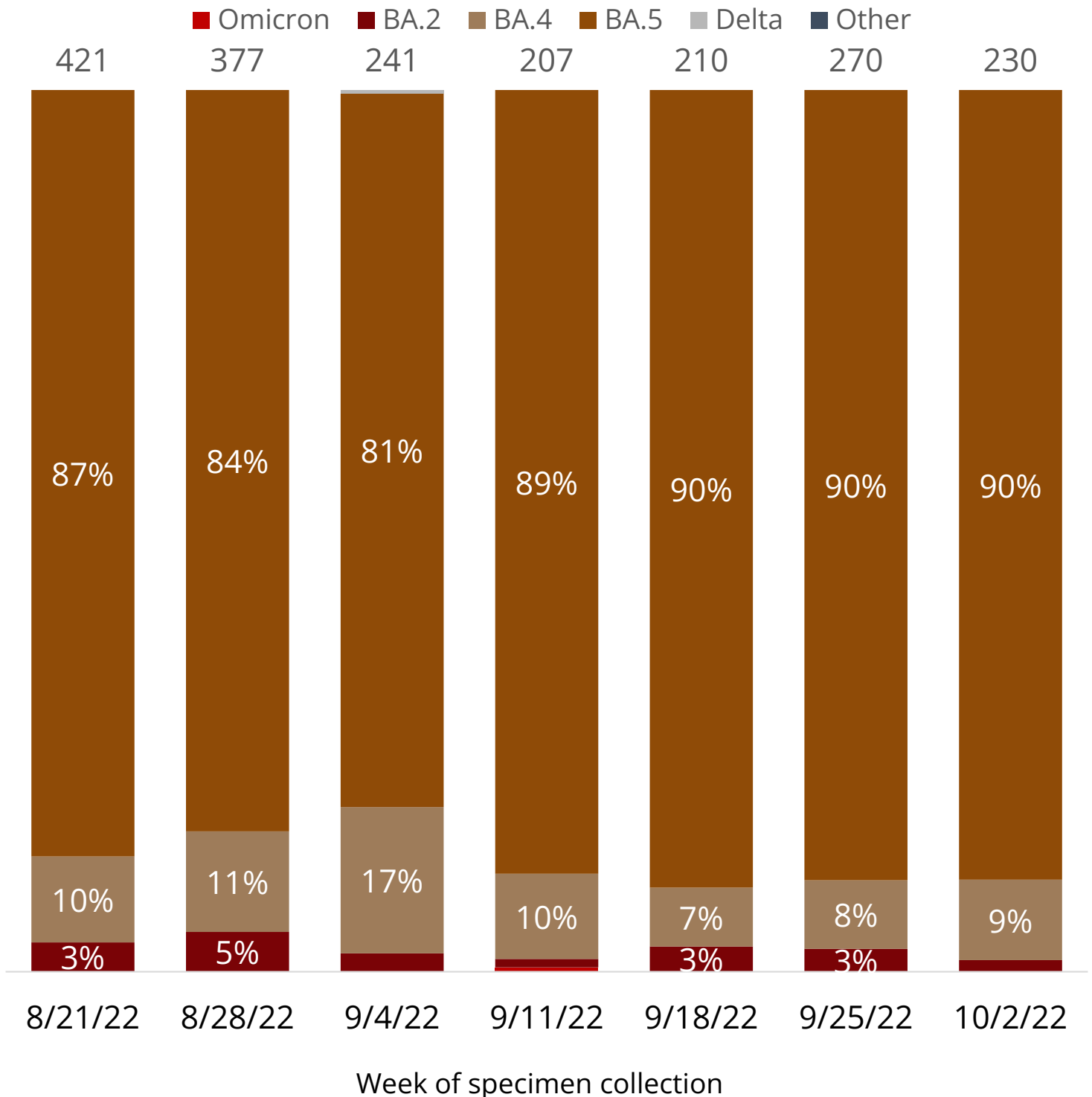


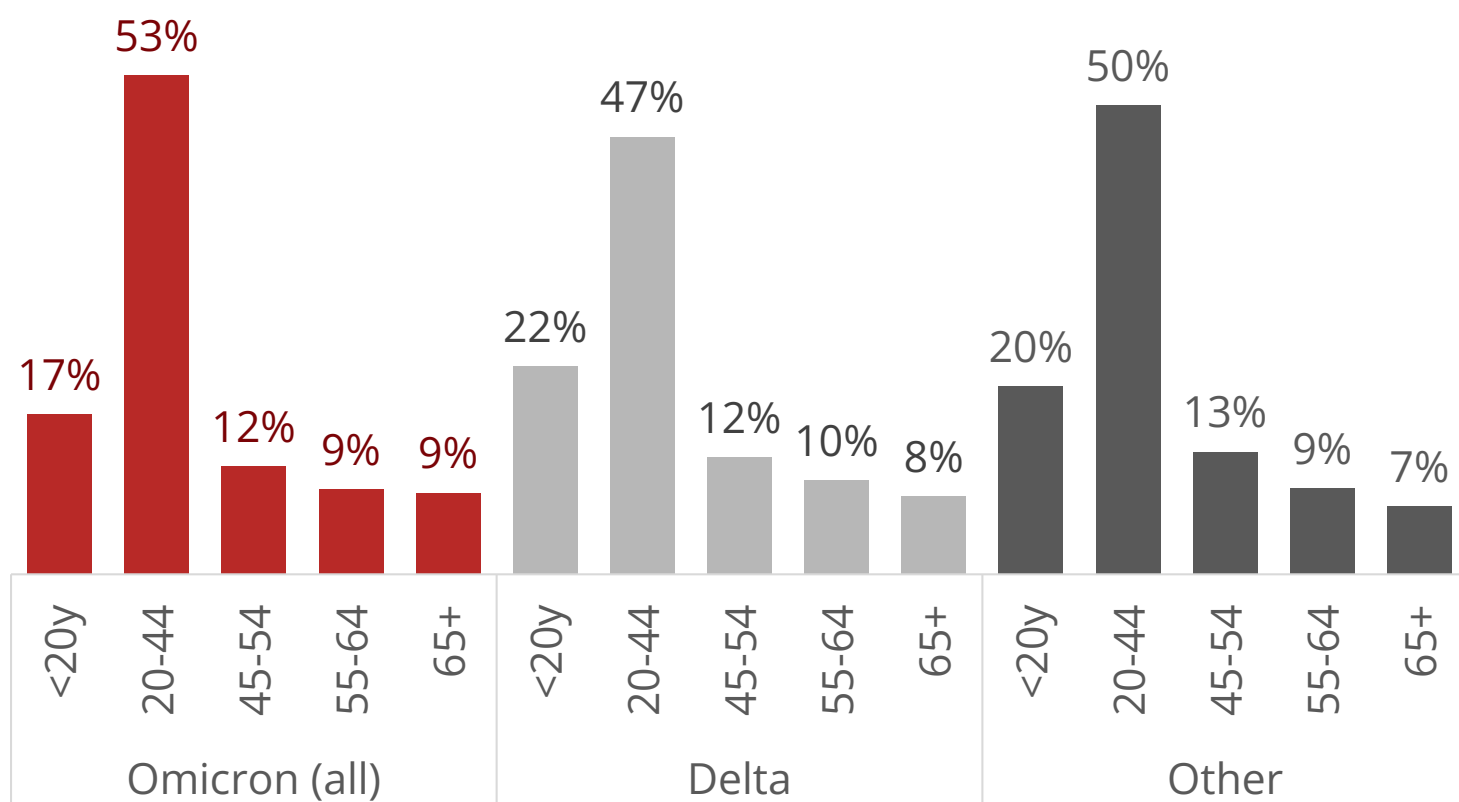


Omicron has been the major circulating variant in Arizona since mid-December 2021. BA.4 and BA.5 became the predominant Omicron sub-variants in June 2022.



Data timeframe represented above: 8/21/2022 to 10/8/2022

Sequenced COVID-19 cases, by variant, for each age group and county



County of Residence	Omicron (other)	Omicron BA.2	Delta	Other	Total Sequenced
Apache	40.6%	5.4%	39.4%	14.4%	591
Cochise	44.0%	7.3%	35.4%	13.1%	919
Coconino	43.7%	4.4%	31.9%	19.8%	9,369
Gila	14.2%	3.1%	53.4%	29.2%	260
Graham	29.2%	12.4%	34.5%	23.9%	226
Greenlee	12.2%	7.3%	75.6%	4.8%	41
La Paz	34.1%	12.2%	34.1%	19.5%	41
Maricopa	39.5%	7.7%	32.0%	20.4%	60,337
Mohave	26.7%	2.1%	53.5%	17.2%	1,936
Navajo	38.5%	7.2%	40.0%	14.0%	1,287
Pima	33.8%	7.5%	40.9%	16.7%	11,471
Pinal	26.6%	4.0%	46.3%	22.3%	4,108
Santa Cruz	43.6%	5.4%	35.2%	15.7%	477
Yavapai	24.0%	3.9%	56.8%	13.9%	1,374
Yuma	35.0%	3.4%	44.8%	16.4%	1,818
Totals	35,901	6,543	32,984	18,439	94,255

Data timeframe represented above: 1/1/2021 to 10/8/2022

NOTE: BA.2.12 & BA.2.12.1 are included under the BA.2 column.

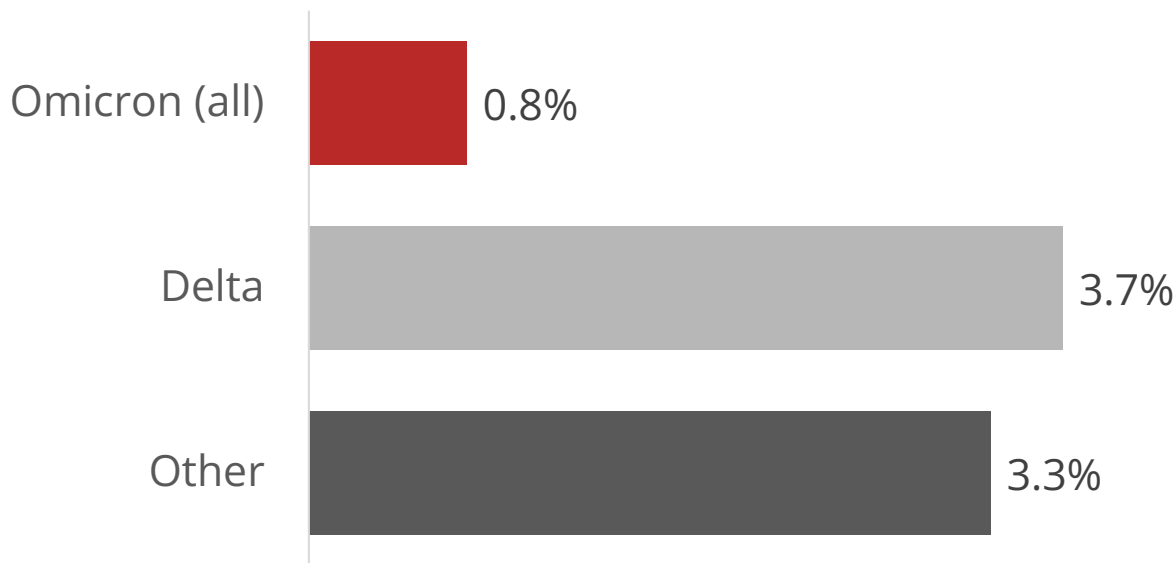
Hospitalizations and deaths of COVID-19 cases, by variant

These graphs show the proportion of sequenced cases for each variant that were hospitalized or died due to COVID-19.

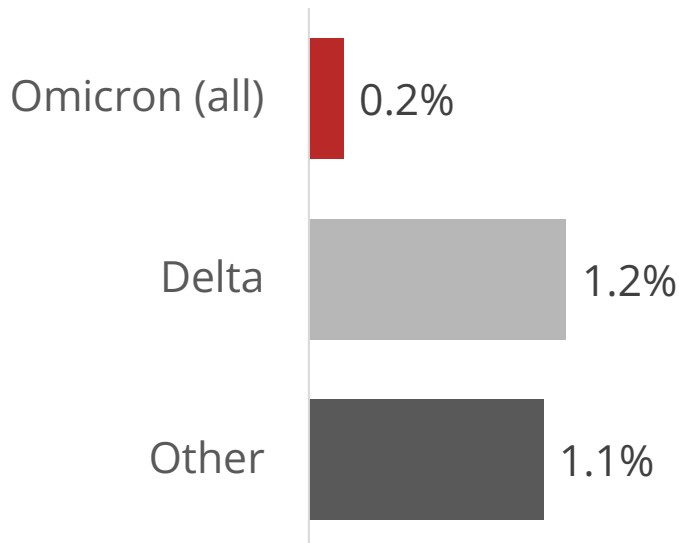
At this time, cases with the Omicron variant were less likely to be hospitalized or die compared to other sequenced cases.

Omicron includes all of its circulating sub-variants in AZ.

Hospitalizations



Deaths

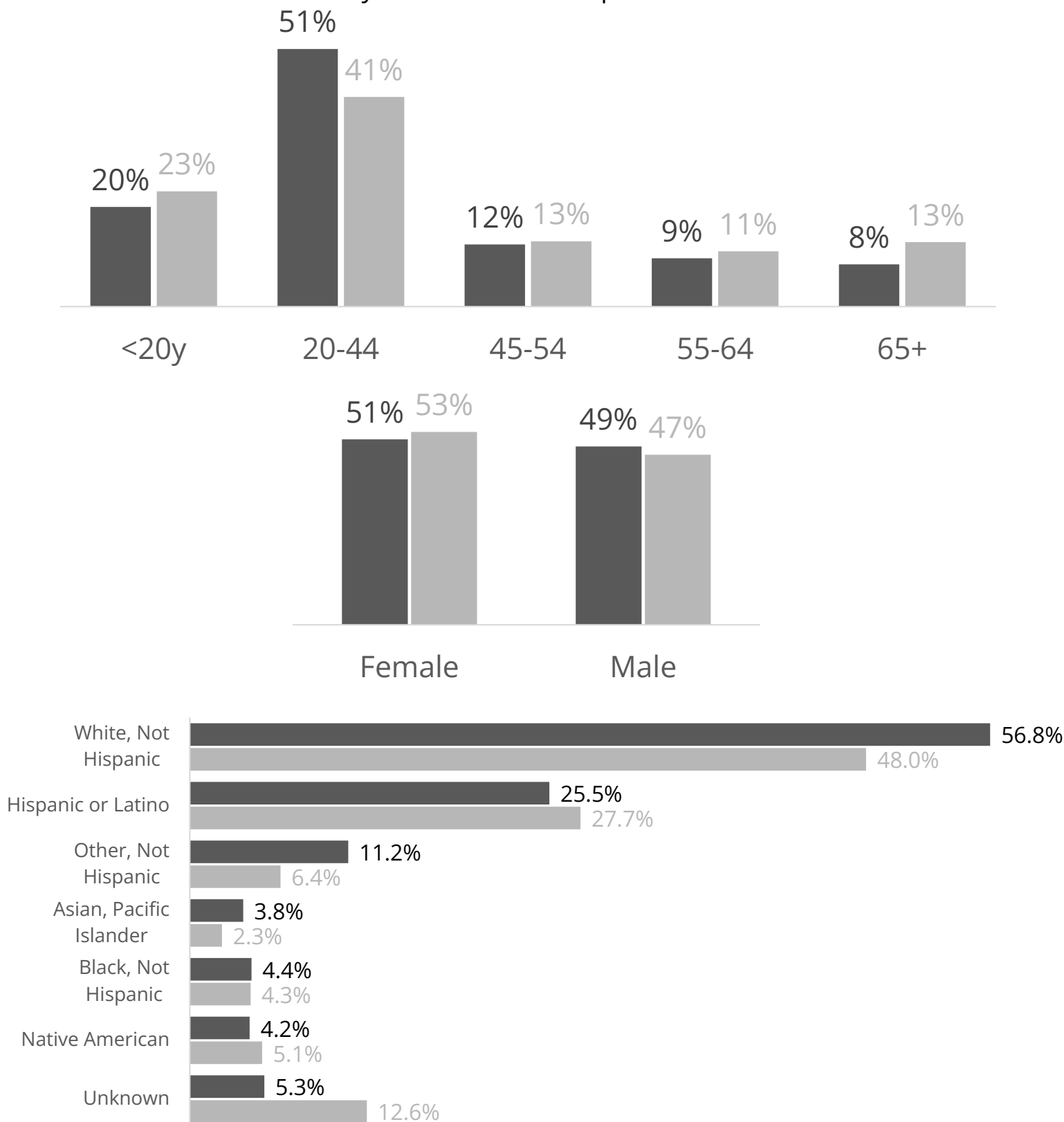


These numbers will change as more information about hospitalizations and deaths is received by ADHS for sequenced cases.

Data timeframe represented above: 1/1/2021 to 10/8/2022

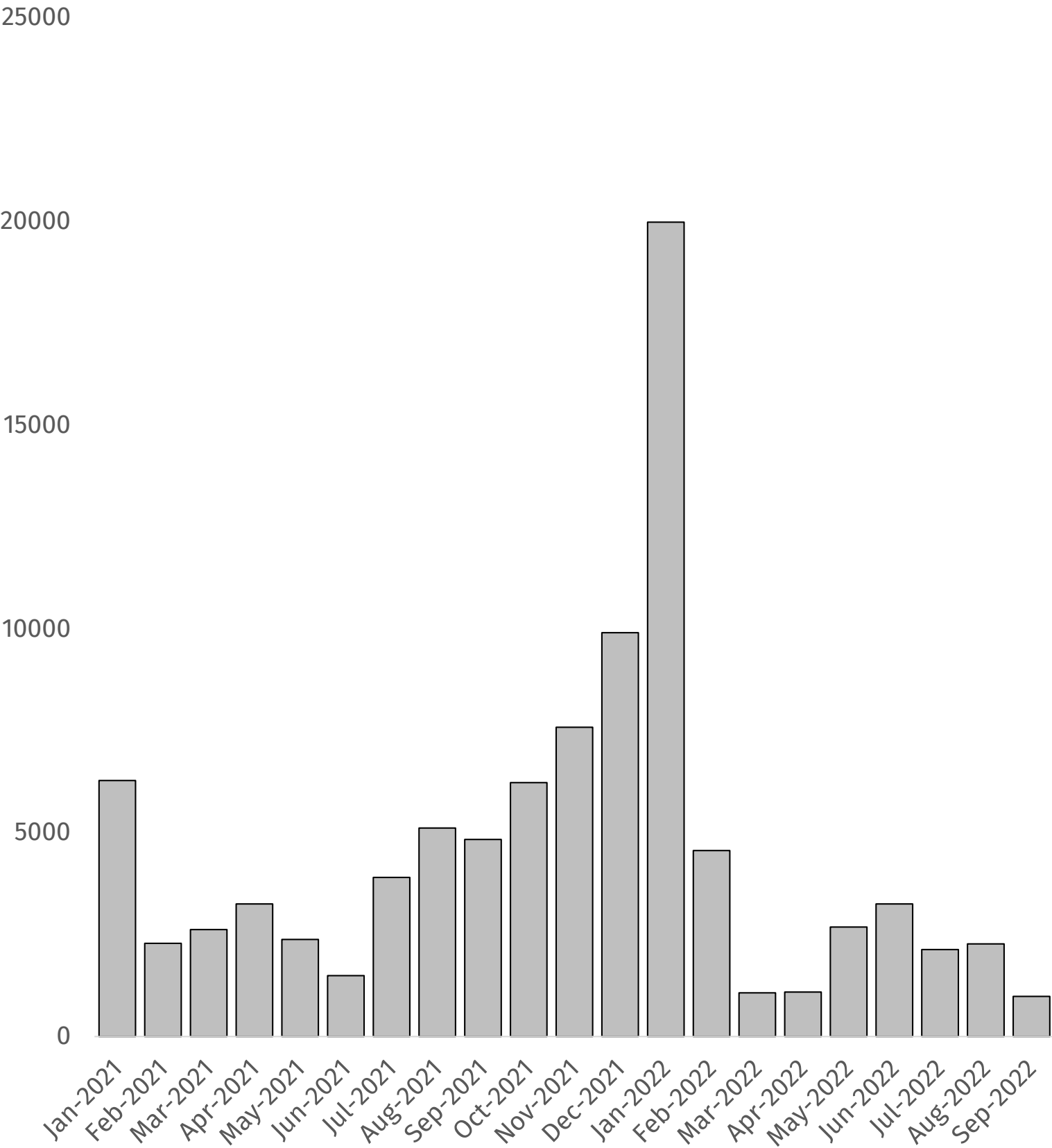
Proportion of COVID-19 cases sequenced compared to case demographics

Demographics for Arizona's sequenced cases resemble those for all 2021 through October 8, 2022 COVID-19 cases, although a higher proportion of cases aged 20-44 years have been sequenced.



Data timeframe represented above: 1/1/2021 to 10/8/2022

Number of COVID-19 cases sequenced, by month of specimen collection



Data timeframe represented above: 1/1/2021 to 9/30/2022

About the data:

- Facilities performing laboratory tests for COVID-19 report positive COVID-19 test results to ADHS pursuant to Arizona Administrative Code R9-6-204.
- Laboratories collect specimens from across the state. Sequencing is performed by specialized laboratories on a sample of specimens. The sequencing results are sent to ADHS and matched to case data.
- The sequencing data shown in this report represent lineage data that has been matched to reported and confirmed COVID-19 cases. Only one sequencing result is shown for a case with multiple results.
- The data timeframe on page 1 (cases with sequenced specimens collected August 21, 2022 to October 8, 2022) was selected to show the prevalence of Omicron and its sub-variants BA.4 and BA.5.
 - BA.2 includes all sub-variants (BA.2.3, BG.2, BN.1, etc.).
 - BA.4 and BA.5 include all sub-variants respectively (BF.1, BE.1, etc.).
- The remainder of the report includes the total accumulated cases with sequenced specimens collected January 1, 2021 to October 8, 2022.
 - This data was compiled, verified, and matched by ADHS .
- Sequencing data is derived from whole genome sequencing performed on a proportion of positive COVID-19 samples in Arizona. Not every positive sample for COVID-19 is sequenced.
- ADHS receives data from various partners, affecting the timing of when summarized sequencing data will be available for any given period. Samples are collected, tested for COVID-19, delivered to the respective laboratories then sequenced. ADHS partners validate the quality of the data and report the results. There is time between each step of the process for matching sequence data to case data.
- COVID-19 sequencing data is reported to ADHS at a rapid rate. Interpretation of the data presented should consider that sequencing data is continuously updated.
- Please consult with public health if making clinical decisions based on circulating variant proportions.